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Original Paper

SUPPLEMENTARY DATA

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Conformational stability and activity analysis of two hydroxymethylbilane synthase mutants, K132N and V215E, with different phenotypic association with acute intermittent porphyria

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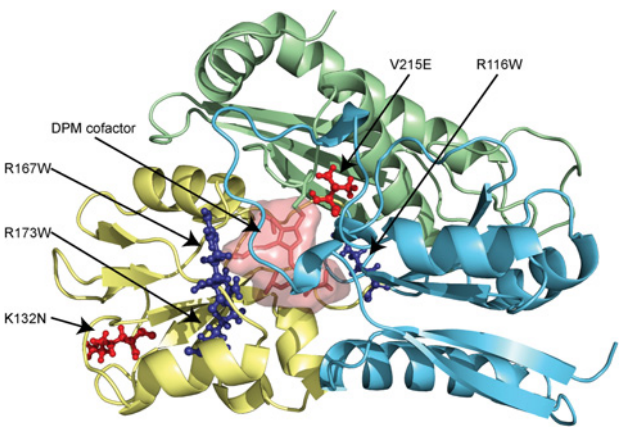

Figure S1 Structural model of HMBS

The location of the two novel mutations studied in this work, K132N and V215E, are presented as ball-and-sticks in red, whereas the three previously reported mutations (R116W, R167W and R173W) are presented as ball-and-sticks in dark blue. The complete structural model of HMBS was constructed with Modeller [1] based on multiple templates (PBD IDs: 1AH5, 1PDA, 1GTK, 1YPN, 3ECR and 3EQ1). Coordinates for residues 55–75 have been issued to loop optimization constructing a large set of possible confirmations. The lowest energy structure was chosen, and further refined with energy minimization using Amber 10 [2].

REFERENCES

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